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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

0 0 0 0 0 0 0 0 0 0	Result
778 775 775 679 625 620 620 343	Score
53.1 52.9 46.3 42.7 42.3	Query Match 1
1017 97 1223 97 1227 91 816 97 160939 76 1514 97 1514 97 590 93	Query Match Length DB
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HSU38784 HSU61397 BC006462 HSU67122 AC079354 AR087051 HSU83117 HSU83117	ID
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98; Conservative 0; Mismatche
                                                                                                                                                                                                                                Submitted (16-OCT-1995) Zhiyuan Shen, Life Sciences Division, Los Alamos National Lab, MS M888, Los Alamos, NM 87545, USA
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                                                     /Protein_d="AAC50733.1"
/Protein_d="AAC50733.1"
/db_xref="GI:1574948"
/translation="MSDQEAKPSTEDLGDKKEGEYIKLKVIGQDSSEIHFKVKMTTHL
KKLKESYCQRQGVPMNSLRFLFEGQRIADNHTPKELGMEEEDVIEVYQEQTGGHSTV"
a 180 c 213 g 314 t
                                                                                                                                                        /note="This cDNA was cloned with the yeast two hybrid system. The protein interacts with human RAD51 and RAD52 proteins in yeast"
                                                                                                                             /note="similar to ubiquitin and to yeast Smt3p (suppressor of MIF2); Method: conceptual translation supplied by
                                                                                                                           author"
                                                                                                                  /codon_start=1
                                                                                                                                                                                             /organism="Homo sapiens"
/db_xref="taxon:9606"
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/protein_id="AAB40388.1"
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/KKLKESYCQROGYPMNSLRFLFEGQRIADNHTPKELGMEEEDVIEVYQEGTGGHSTV"
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                                                                                                                                                                                                       Steven Jones, Jennifer Asano, Ian Bosdet, Yaron Butterfield, Susanna Chan, Readman Chiu, Chris Fjell, Erin Garland, Ran Guin, Letticia Hsiao, Martin Krzywinski, Reta Kutsche, Oliver Lee, Soo Sen Lee, Victor Ling, Carrie Mathewson, Candice McLeavy, Steven Ness, Pawan Pandoh, Anna-Liisa Prabhu, Parvaneh Saeedi, Jacqueline Schein, Duane Smailus, Michael Smith, Lorraine Spence, Jeff Stott, Michael Thorne, Miranada Tsai, Natasia, vana den Bosch, Jill Vardy, Cachero Vana Goatte Thomas, Miranada Tsai, Natasia, Vana den Bosch, Jill Vardy, Cachero Vana Goatte Thomas, Miranada Tsai, Natasia, Vana den Bosch, Jill Vardy, Cachero Vana Goatte Thomas, Miranada Tsai, Natasia, Vana den Bosch, Jill Vardy, Cachero Vana Goatte Thomas, Miranada Tsai, Natasia, N
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Contact: Robert Strausberg, Ph.D.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BC006462.1 GI:13623670
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through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Series: IRAL Plate: 8 Row: f Column: 12.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                       George Yang,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           info@bcgsc.bc.ca
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/organism="Homo sapiens"
/db_xref="LocusID:7341"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Direct Submission
Submitted (16-AUG-1996) Department of Cell Biology, The Scripps
Submitted (16-AUG-1996) Department of Cell Biology, The Scripps
Submitted (16-AUG-1996) Department of Cell Biology, The Scripps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 (bases 1 to 816)
Mahajan,R., Delphin,C., Guan,T., Gerace,L. and Melchior,F.
A small ubiquitin-related polypeptide involved in targetin
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                                                                                                                     /product="SUMO-1"
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a 153 c 173 g 255 t
                                                                                                                                                                                                                                                       /note="conjugated post-translationally to RangAP1; ubiquitin-related protein; similar to UBL1 encoded by GenBank Accession Number U38784, PIC1 encoded by GenBank Accession Number U61397 and GMP1 encoded by GenBank Accession Number U72722"
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                                                                                                                                                                                                                                                                                                                                                                      /clone="IMAGE Consortium Clone ID: 49768, 51818,
                           46.3%;
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                                2 (bases 1 to 160939)
Waterston, R.H.
Direct Submission
                                                                                                                                                                                                                                                                      SEQUENCE, 11 unordered pieces. AC079354
                                                                                                                                                                                                                                                                                                         Homo sapiens chromosome UNK clone RP11-1145F21, WORKING DRAFT
Submitted (28-AUG-2000) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. Louis,
                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                             AC079354
                                                                                     Unpublished
                                                                                                      The sequence of Homo sapiens clone
                                                                                                                             Waterston, R.H.
                                                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                                    HTG; HTGS_PHASE1; HTGS_DRAFT.
                                                                                                                                                                                                                                                         AC079354.1 GI:9931967
                                                                                                                                              (bases
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       * NOTE: This is a 'working draft' sequence. It currently consists of 11 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Center project name: H_NH1145F21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Center: Washington University Genome Sequencing Center Center code: WUGSC
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Sequencing vector: plasmid; 0%
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                                                                /note="assembly_name:Contig14" 65844 . .83507
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10619. .21836
                                                                                                                                                                                                                                                                                                                          /db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                          /organism="Homo sapiens"
                                    83608. .105339
                                             /note="assembly_name:Contig15"
                                                                                                                                                                                                /note="assembly_name:Contig12
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                                                                                                                                                                                                                                                                                                                                                                                                Location,
                 /note="assembly_name:Contig16
                                                                                                                                                                                                                                                                                                                                                                                                               83607: gap of unknown length
105339: contig of 21732 bp in length
105439: gap of unknown length
105439: gap of unknown length
143858: contig of 38419 bp in length
143958: gap of unknown length
147000: contig of 3042 bp in length
151655: contig of 3042 bp in length
151755: gap of unknown length
151755: gap of unknown length
160939: contig of 9184 bp in length.
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contig of 11218 bp in length
gap of unknown length
contig of 13673 bp in length
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                                                                                                                      ccaaaagaagaggaatatcaggttgaagtcaagatgacagataaggtgagagtaatgact 923
GAATACAACAGAACACTGCTCTTTT 138332
                                                         GAAGATCCCAGAAAAGTTCTAATTTTCATTAGCAATTAATAAAGCTATACATGCAGAAAT 138358
                                                                                                                                                                                    CCAAAAGAAGAAGAATATCAGGTTGAAGTCAAGATGACAGATAAGGTGAGAGTAATGACT 138478
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147101. .151655
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a 35217 c 34748 g 43792 t 1003 others
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143959. .147000
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                                                                                                       attattgtttgttttcattgtgctgatttttggtgatcaagcctcagtccccttcatatt 601
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Baker, B.F. and Cowsert, L.M.
Antisense modulation of Sentrin expression
Patent: US 598564-A 1 16-NOV-1999;
Location/Qualifiers
1. .1514
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AR087051
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Okura,T., Gong,L., Kamitani,T., Wada,T., Okura,I., Wei,C.-F.,
Okura,T., Gong,L., Kamitani,T., Wada,T., Okura,I., Wei,C.-F.,
Chang,H.-M. and Yeh,E.T.H.
Okura,T., Gong,L., Kamitani,T., Wada,T., Okura,I., Wei,C.-F.,
Chang,H.-M. and Yeh,E.T.H.
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                                                    CTGATAATCATACTCCAAAAGAACTGGGAATGGAGGAAGAAGATGTGATTGAAGTTTATC 409
                                                                 ctgataatcatactccaaaagaactgggaatggaggaagaagatgtgattgaagtttatc 361
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (23-DEC-1996) Division of Molecular Medicine, Department
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Blvd., Suite 900, Houston, TX 77030, USA
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/db_xref="taxon:9606"
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X99586
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (26-JUL-1996) P. Chiurazzi, Universita' Cattolica largo F. Vito 1, I- 00168 Roma, ITALY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 (bases 1 to 590)
Lapenta, V., Chiurazzi, P., van der Spek, P., Pizzuti, A., Hanaoka, F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
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                                                                 /db_xref="SWISS-PROT:093068"
/translation="MSDQEARPSTEDLGDKKEGEVIKLKVIGQDSSEIHFKVKMTHL
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KKLKESYCQRQGVPMNSLFFLFEGGRIADNHTPKELGMEEEDVIEVYQEQTGGHSTV"
KKIKESYCQRQGVPMNSLFFLFEGGRIADNHTPKELGMEEEDVIEVYQEQTGGHSTV"
                                                                                                                                                                                                               protein"
                                                                                                                                                                                                                                                                                                  /tissue_type="brain"
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                                                                                                                                                                                                                                                                                                                                   /dev_stage="foetus"
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                                                                                                                                                                                                                                                                                  /gene:
                                                                                                                                                            /product="SMT3C protein"
                                                                                                                                                                                            /note="ubiquitin-like protein"
                                                                                                                                                                                                                             function="suppressor of MIF2 which encodes a centromere
                                                                                                                                                                                                                                               /gene="SMT3C"
                                                                                                                                          /protein_id="CAA67898.1"
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                                                               121 GGATAAGAAGGAAGGTGAATATATTAAACTCAAAGTCATTGGACAGGATAGCAGTGAGAT 180
                                                                                  129 ggataagaagcaaggtgaatatattaaactcaaagtcattggacaggatagcagtgagat 188
                                                                                                                                61 GGGTGAAGCCACCGTCATCATGTCTGACCAGGAGGCAAAACCTTCAACTGAGGACTTGGG 120
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TCACTTCAAAGTGAAAATGACAACACATCTCAAGAAACTCAAAGAATCATACTGTCAAAG
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O'Neill.R. and Palese, P.
Antiviral compounds that inhibit interaction of host cell proteins and viral proteins required for replication patent: EP 0861322-A 18 02-SEP-1998;
MOUNT SINAL MEDICAL CENTER (US)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM
241 GGAATGGAGGAAGAAGATGTGATTGAAGTTTATCAGGAACAAACGGGGGGTCATTCAACA 300
                  328 ggaatggaggaagaagatgtgattgaagtttatcaggaacaaacggggggtcattcaaca 387
                                                                    181 TCACTCAGGTTTCTCTTTGAGGGTCAGAGAATTGCTGATAATCATACTCCAAAAGAACTG
                                                                                    268 tcactcaggtttctcttttgagggtcagagaattgctgataatcatactccaaaagaactg
                                                                                                                                                                                       208
                                                                                                                                                                                                                          148 tatattaaactcaaagtcattggacaggatagcagtgagattcacttcaaagtgaaaatg 207
                                                                                                                                                                                                        61 TATATTAAACTCAAAGTCATTGGACAGGATAGCAGTGAGATTCACTTCAAAGTGAAAATG 120
                                                                                                                                                                                                                                                                                            88 atytctgaccaggaggcaaaaccttcaactgaggacttgggggataagaagcaaggtgaa 147
                                                                                                                                                                                                                                                                          Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           301 TCATACTCCAAAAGAACTGGGAATGGAGGAAGAAG 335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               309 tcatactccaaaagaactgggaatggaaggaag 343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ACAACACATCTCAAGAAACTCAAAGAATCATACTGTCAAAGACAGGGTGTTCCAATGAAT 180
                                                                                                                                                        acaacacatctcaagaaactcaaagaatcatactgtcaaagacagggtgttccaatgaat 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Direct Submitted (27-SEP-1996) Laboratory of Cell Biology, R Thimmareity. 1230 York Avenue, New York, NY 10021, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matunis,M.J., Coutavas,E. and Blobel,G.
A novel ubiquitin-like modification modulates the partitioning of
the ran-GTPase-activating protein RangAP1 between the cytosol and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matunis, M.J., Coutavas, E. and Blobel, G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       97133418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 306)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          U72722.1 GI:1703502
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human gap modifying protein 1 mRNA, complete cds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HSU72722
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (bases 1 to 306)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                112 a
                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           _Biol. 135 (6 Pt 1), 1457-1470 (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                            /translation="msDQEAKPSTEDLGDKKEGEYIKLKVIGQDSSEIHFKVKMTTHL
KKLKESTCORQGVPMNSLRFLFEGQRIADNHTPKELGMEEEDVIEVYOEQTGGHSTV"
48 c 75 g 71 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="GMP1; covalently associated with Ran GTPase
activating protein RanGAP1; ubiquitin-like protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /product="gap modifying protein 1"
/protein_id="AAB40390.1"
/db_xref="GI:1703503"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /cel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                 17.4%; Score 255; DB 97; 99.7%; Pred. No. 5.2e-117;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                _line="HeLa"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            306 bp
                                                                                                                                                                                                                                                                                                                                                       0;
                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          mRNA
                                                                                                                                                                                                                                                                                                                                                                                 Length 306;
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                                                                                                                                                                                                                                                                                                                                                0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rockefeller
                                                                                                                                                                                                                                                                                                                                            Gaps
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VERSION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LOCUS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   301 GTTTAG 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  388 gtttag 393
                                                                                                                                                              source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Assembly program: XGAP4; version 4.5
Sequencing vector: plasmid; L08752; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Consensus quality: 153015 bases at least Q40
Consensus quality: 153015 bases at least Q30
Consensus quality: 153938 bases at least Q30
Consensus quality: 154565 bases at least Q20
Insert size: 155213; sum-of-contigs
Insert size: 164818; 1.0% error; agarose-fp
Quality coverage: 6.89x in Q20 bases; sum-of-contigs
coverage: 7.27x in Q20 bases; agarose-fp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens chromosome 1 clone RP11-179G5, *** SEQUENCING PROGRESS ***, 8 unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (25-FEB-2001) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 155913)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AL513282
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On reb 28, 2001 this sequence version replaced gi:13161719.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HTG; HTGS_PHASE1; HTGS_DRAFT.
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Center code: SC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   * NOTE: This is a 'working draft' sequence. It currently consists of 8 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: humquery@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Web site: http://www.sanger.ac.uk
                                                                                                                                                                                                                                                                                        20839 20938; gap of 100 bp 50589; contig of 29651 bp in length 50590 50689; gap of 100 bp 50690 81538; contig of 30849 bp in length 81539 81638; gap of 100 bp 81638; gap of 100 bp 100 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             as soon as it is available and the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   be preserved
                                                                                                                                                                                                                                                                 153076 153175: gap of 100 bp
153176 155913: contig of 2738 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     155913 bp
                                                                          /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                            1. .155913
                                                                                                                                                                                                                       Location/Qualifiers
/clone="RP11-179G5"
                                /chromosome="1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20838: contig of 20838 bp in length
138: gap of 100 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Project Information
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Db 136416 GAGGTTCTGCTTACCCGAGGCCGCTGCTGTGCGGAGACCCCCGGGTGAAGCCACTGTCAT 136357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BASE COUNT
                                                                                                                                                                                                          Db 136296 ATATATTAAACTCAAAGTCATTGGACAGGATAGCAGTGAGATTCACTTCAAAGTGAAAAT 136237
                                                                                                                                                                                                                                                                                                                                                                                                                                       Db 136056 AGTTTAGATATTCTTTTTTTTTTTTCTTTTCCCCCAATCCCTT 136012
                                                                                               AL359981/c
             KEYWORDS
                        VERSION
                                                                     DEFINITION
SOURCE
                                          ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches 400;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 10.2%;
Best Local Similarity 98.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                147 atatattaaactcaaagtcattggacagggatagcagtgagattcacttcaaagtgaaaat 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                27 gaggttctgcttacccgaggccgctgctgtgcggagacccccgggtgaagccaccgtcat 86
                                                                                                                                                                               87 catgtctgaccaggaggcaaaaccttcaactgaggacttgggggataagaagcaaggtga 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note-"assembly_fragment:03083
fragment_chain:4"
43830 a 34529 c 35326 g 41527 t
                                                    Homo sapiens chromosome 1 clone RP11-115N23, *** SEQUENCING PROGRESS ***, 7 unordered pieces
                                          AL359981
               HTG; HTGS_PHASE1; HTGS_DRAFT
                            AL359981.10 GI:12331082
                                                                                    AL359981
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
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81639. .8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="assembly_fragment:02750
fragment_chain:3"
149496. 153075
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fragment_chain:1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    89783.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="assembly_fragment:03283
fragment_chain:2"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="assembly_fragment:02743
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         108206.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="assembly_fragment:02486
fragment_chain:4"
fragment_cree;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="assembly_fragment:00942
fragment_chain:3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="assembly_fragment:00478
fragment_chain:2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ragment_chain
                                                                                      167440 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .81538
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                                                                                         DNA
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                                                                                                20-JAN-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Assembly program: XGAP4; version 4.5 Sequencing vector: plasmid; LO8752; 100% of reads Chemistry: Dye-terminator ET-amersham; 16% of reads Chemistry: Dye-terminator Big Dye; 83% of reads
Consensus quality: 165078 bases at least 040
Consensus quality: 165122 bases at least 030
Consensus quality: 16518 bases at least 020
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Insert size: 166840; sum-of-contigs
Insert size: 138972; 3.5% error; agarose-fp
Quality coverage: 6.32x in Q20 bases; sum-of-contigs Quality
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  coverage: 8.08x in Q20 bases; agarose-fp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Center project name: bA115N23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Web site: http://www.sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      On Jan 22, 2001 this sequence version replaced gi:10186747
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (20-JAN-2001) Sanger Centre, Hinxton, Cambridgeshire, CB10 ISA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NOTE: This is a 'working draft' sequence. It currently consists of 7 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Center code:
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129133 132599: contig of 3467 bp in length
132600 132699: gap of 100 bp
132700 141603: contig of 800 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           125181 125280: gap of 100 bp 125281 129032: contig of 3752 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       141504 141703: gap of 100 bp
141704 167440: contig of 25737 bp in length.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              34811 34910: gap of 100 bp
34911 125180: contig of 90270 bp in length
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18092 348
/note="assembly_fragment:00856
fragment_chain:1"
                                                /note="assembly_fragment:01240
fragment_chain:1"
129133. .132599
                                                                                                                                                                                               34911.
                                                                                                                               /note="assembly_fragment:03000
fragment_chain:1"
                                                                                                                                                                                                              /note="assembly_fragment:02116
fragment_chain:1"
                                                                                                                                                                                                                                                                 18092. .34810
                                                                                                                                                                                                                                                                                                                                                                                                                          /db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                       note="assembly_fragment:00134
                                                                                                                                                                                                                                                                                                                                                          /clone_lib="RPCI-11.1"
                                                                                                                                                                                                                                                                                                                                                                                       /clone="RP11-115N23"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Homo sapiens"
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391: gap of 100 bp
34810: contig of 16719 bp in length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VERSION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            327 gggaatggaggaagaagatgtgattgaagttttatcaggaacaaacggggggtcattcaac 386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         267 ttcactcaggtttctctttgagggtcagagaattgctgataatcatactccaaaagaact 326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         207 gacaacacatctcaagaaactcaaagaatcatactgtcaaagacagggtgttccaatgaa 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          147 atatattaaactcaaagtcattggacaggatagcagtgagattcacttcaaagtgaaaat 206
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         27 gaggttctgcttacccgaggccgctgctgtgcggagacccccggggtgaagccaccgtcat 86
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www-shgc.stanford.edu
Quality: Phrap Quality >=40 99.8% of Sequence;
Estimated Total Number of Errors is 0.3.
                                                    Finishing Completed at Stanford Human Genome Center
                                                                                                                Submitted (29-APR-2000) DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
On Apr 29, 2000 this sequence version replaced 91:7021594.
                                                                                        www.jgi.doe.gov
                                                                                            Draft Sequence Produced by DOE Joint Genome Institute
                                                                                                                                                                                                                                Submitted (07-OCT-1999) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, US (bases 1 to 106168)
                                                                                                                                                                                               DOE Joint Genome Institute and Stanford Human Genome Center.
                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 106168)

DOE Joint Genome Institute and Stanford Human Genome Center.
                                                                                                                                                                                         Direct Submission
                                                                                                                                                                                                                                                                                              Direct Submission
                                                                                                                                                                                                                                                                                                              DOE Joint Genome Institute.
                                                                                                                                                                                                                                                                                                                                                          Unpublished
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/note="assembly_fragment:00528"
141704. .167440
/note="assembly_fragment:02701"
a 37675 c 35802 g 45906 t
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PKI

19 clone CTC-30107, complete sequence.
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1 (bases 1 to 178733)

Abola,A.P., Bruno,D., Conn,L., Dela Rosa,M., Faulkner,D., Abola,A.P., Glukhov,S., Hansen,N., Herman,Z.S., Hyman,R., Federspiel,N., Glukhov,S., Hansen,N., Morehouse,A.J., Nguyen,M., Mao,J., Lam,B., Marathe,R., Miranda,M., Morehouse,A.J., Nguyen,M., Oefner,P., Palm,C.J., Ramirez,D., Southwick,A.M., Wilhelmy,J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens chromosome 19 clone RP11-50111, WORKING DRAFT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 (bases 1 to 178733)
2 (bases 1 to 178733)
Abola,A.P., Bruno,D., Conn,L., Dela Rosa,M., Faulkner,D., Federspiel,N., Glukhov,S., Hansen,N., Herman,Z.S., Hyman,R., Mao,J., Marathe,R., Morehouse,A.J., Oefner,P., Palm,C.J.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE, 15 unordered pieces.
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                                                                                                                                                                                                                                                                                                                                                                                    On Mar 8, 2001 this sequence version replaced gi:13236646.
                                                                                                                                                                                                                                                                                                                                                                                                                                Direct Submission

Submitted (09-MAY-2000) DNA Sequencing and Technology Center, Stanford University, 855 California Avenue, Palo Alto, CA 94304,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AC068786.11 GI:13249431
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ramirez,D., Wilhelmy,J., Yu,S. and Davis,R.W.
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                  Sequencing Vector: M13mp18; X02513
Chemistry: Dye-primer; 0% of reads
Chemistry: Dye-terminator Big Dye; 100% of r
Assembly program: Phrap; version 0.990319
Consensus quality: 168546 bases at least Q40
Consensus quality: 171030 bases at least Q30
Consensus quality: 172366 bases at least Q20
                                                                                                                                                                                                                                Center project name: 899
Center clone name: RP11-50I11
Center clone name: RP11-50II1
                                                                                                                                                                                                                                                                                                                                           Center: Stanford DNA Sequencing and Technology Development
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  and Davis, R.W.
                                                                                                                                                                                                                                                                                                    Center code: SDSTDC
Insert size: 178045; agarose-fp
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/db_xref="taxon:9606"
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100.0%; Pred. No. 5.9e-38;
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Quality coverage: 9.2x in Q20 bases; agarose-fp
Quality coverage: 9.2x in Q20 bases; sum-of-contigs.
* NOTE: This is a 'working draft' sequence. It currently
* NOTE: This is a 'working draft' sequence in the pieces
* consists of 15 contigs. The true order of the pieces
* is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   * arbitrary. Gaps between the contigs are represented as

* runs of N, but the exact sizes of the gaps are unknown

* This record will be updated with the finished sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   be preserved.
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   /note="assembly_name:Contig40"
92285. .114445
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7766 .11506
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                                                                                                      /note="assembly_name:Contig38
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                                                                                                                                       /note="assembly_name:Contig37"
                                                     /note="assembly_name:Contig39"
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114545: gap of unknown length
140410: contig of 25865 bp in length
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gap of unknown length
contig of 1619 bp in length
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contig of 14892 bp in length
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contig
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contig of 3741 bp in length
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TITLE
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                                                                                                                   Center project name: H_NHO686006

Sequencing vector: M13: 100%
Sequencing vector: plasmid; 0%
Chemistry: Dye-primer ET; 100% of reads
Chemistry: Dye-terminator Big Dye; 0% of reads
Chemistry: Dye-terminator Big Dye; 0% of reads
Chemistry: Dye-terminator Big Dye; 0% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 173047 bases at least 040
Consensus quality: 176179 bases at least 030
Consensus quality: 178311 bases at least 020
Insert size: 191000; agarose-fp
Insert size: 191000; agarose-fp
Quality coverage: 5.44 in 020 bases; sum-of-contigs
Quality coverage: 5.45 in 020 bases; sum-of-contigs
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                                                                                                                                                                                                                                                                                                                                                                            Web site:http://genome.wustl.edu/gsc/index.shtml
                                                                                                                                                                                                                                                                                                                                                                                                Center: Washington University Genome Sequencing Center Center code: WUGSC
                                                                                                                                                                                                                                                                                                                                                                                                                                                     MO 63108, USA On Aug 17, 2000 this sequence version replaced gi:7801500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (22-APR-2000) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St.
     NOTE: This is a 'working draft' sequence. It currently consists of 17 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Waterston, R.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The sequence of Homo sapiens clone
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Homo sapiens chromosome 2 clone RP11-68606, WORKING DRAFT SEQUENCE,
17 unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unpublished
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ture 140511. 178733
/note="assembly_name:Contig43"
50350 a 40923 c 42172 g 43887 t ]
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    Project

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Pred. No.
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. 5.9e-38;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1. .181861
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95028: contig of 16761 bp in length
95128: gap of unknown length
127606: contig of 32478 bp in length
127706: gap of unknown length
181861: contig of 54155 bp in length
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21574: contig
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12401: contig
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1769: gap of unknown length
3011: contig of 1242 bp in length
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contig of 9172
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Matches 101861;
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; SEQ ID NO 1
; LENGTH: 1514
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAMEXKEY: CDS
; LOCATION: (136)..(441)
US-09-213-768-1
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                                                                                                                                                                                                                                                                                                                                                                  Minimum DB seq length: 0
Maximum DB seq length: 2000000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Total number of hits satisfying chosen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Word size
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Scoring table:
                                                                                                                                                                                                                                                                                                               Post-processing: Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Searched:
pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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                                                                                                            Issued_Patents_NA:*
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5: /cgn2_6/ptodata/2,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     324599 seqs, 94655562 residues
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cgggaaggatttgtaaaccc.....gataaatgggcatgccagcc 1465
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/cgn2_6/ptodata/2/ina/5B_COMB.seq:*
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   parameters:
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SUMMARIES Result Query No. Score Match Length DB ID Description

ALIGNMENTS

620

42.3

1514 2

us-09-213-768-1

Sequence 1, Appli

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US-09-213-768-1
US-09-213-768-1
; Sequence 1, Application US/09213768
; Patent No. 598564
; Patent No. 598564
; GENERAL INFORMATION:
APPLICANT: Brenda F. Baker
; APPLICANT: Lex M. Cowsert
; APPLICANT: Lex M. Cowsert
; TITLE OF INVENTION: ANTISENSE MODULATION OF SENTRIN EXPRESSION
FILE REFERENCE: RTS-0026
; CURRENT APPLICATION NUMBER: US/09/213,768
; CURRENT FILING DATE: 1998-12-17
; NUMBER OF SEQ ID NOS: 47
; SEQ ID NO 1
; LENGTH: 1514
; TYPE: DNA
ORGANISM: HOMO Saniens
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Search completed: August 17, 2001, 11:20:01 Job time: 6356 sec

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Best Local Similarity 99.9%;
Matches 670; Conservative
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                                                                                                                    482 aaaactggcaccccatctctttgaaacatctggtaatttgaattctagtgctcattattc
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                662 ttttcaggctt 672
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ttttcaggctt 720
                                           accetetecetttttaaaaattacgtgtgcacagagaggtcacctttttcaggacattgca
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                                     acceteteettttaaaaattaegtgtgeacagagaggteacettttteaggaeattgea
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Pred. No. 4.2e-279;
0; Mismatches 1; Indels
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OM nucleic - nucleic search, using sw model
                                                     Run on:
August 17, 2001, 10:09:15; Search time 131.18 Seconds (without alignments) 7012.318 Million cell updates/sec
                                                                                                                                                                                    GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd
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Scoring table: Sequence: Perfect score: US-09-484-964-1 cgggaaggatttgtaaaccc.....gataaatgggcatgccagcc 1465

Searched: 730101 seqs, 313950809 residues

Gapop 60.0 ,

Gapext 60.0

Word size : 50

Total number of hits satisfying chosen parameters:

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Minimum DB seg length: 0
Maximum DB seg length: 2000000000

Post-processing: Listing first 45 summaries

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() /SIDSI/gcgdata/geneseq/geneseqn/NA199 DAT: * /SIDS1/gcgdata/geneseq/geneseqn/NA1982.DAT:* /SIDS1/gcgdata/geneseq/geneseqn/NA1983.DAT:* /SIDS1/gcgdata/geneseq/geneseqn/NA1980.DAT:* /SIDS1/gcgdata/geneseq/geneseqn/NA1981.DAT:* /SIDS1/gcgdata/geneseq/geneseqn/NA1985.DAT:*/SIDS1/gcgdata/geneseq/geneseqn/NA1986.DAT:* /SIDS1/gcgdata/geneseq/geneseqn/NA1984.DAT:* /SIDS1/gcgdata/geneseq/geneseqn/NA1987 /SIDS1/gcgdata/geneseq/geneseqn/NA1998.DAT:*
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/SIDS1/gcgdata/geneseq/geneseqn/NA2001.DAT:* .DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

0

40045086	Result
1465 895 895 620 300 284 284 197	Score
100.0 61.1 61.1 42.3 20.5 19.4 19.4 13.4	% Query Match
1465 1196 1220 1514 616 372 372 372 180	% Query Match Length DB
19 19 19 21 21 18 22 22 17	
AAV34564 AAV59572 AAV59557 AAZ35859 AAAA16215 AAT63339 AAF59399 AAF59399 AAT03735	ID
Homo sapiens sentr Human secreted pro Human secreted pro Human sentrin nucl Human sentrin nucl Human host cell pr Human host cell pr TNF-R p55IC/Fas-IC Human gene signatu	Description

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ALIGNMENTS

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sentrin-1; protection; tumour necrosis factor; tnf; apoptosis;
Fas/APO-induced; tumour cell death; induction; tumour aggressi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAV34564;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11-SEP-1998
                                                                                                                                                                                                                                                                                             The sequence is that encoding the sentrin-1 polypeptide. Sentrin polypeptides have the ability to protect or guard cells from tumour necrosis factor (TNF) or Fas/APO induced cell death (apoptosis). Inhibitors of the sentrin polypeptides, e.g. antibodies, can be used for inducing cell death, e.g. antibodies. The products can also be used for particularly in tumours. The products can also be used for determining the aggressiveness of a tumour and for detection and isolation of products. The sentrin polypeptide can also be used to detect a ubiquitin conjugating enzyme polypeptide or PML polypeptide.
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P-PSDB; AAW60079.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 10; Page 76-77; 120pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New isolated sentrin polypeptide(s) - which inhibit TNF receptor or Fas/APO-induced apoptosis, used to develop products for inducing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Yeh ETH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (TEXA ) UNIV TEXAS SYSTEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     05-NOV-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cell death in tumours
                                                                                                                                                                                                                                                                    Sequence 1465 BP; 455 A; 248 C; 292 G; 470 T; 0 other;
121 gacttgggggataagaagcaaggtgaatatattaaactcaaagtcattggacaggatagc 180
               121 gacttgggggataagaagcaaggtgaatatattaaactcaaagtcattggacaggatagc 180
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                                                                            61 agacccccgggtgaagccaccgtcatcatgtctgaccaggaggcaaaaccttcaactgag 120
                                                                                                                                          1 cgggaaggatttgtaaaccccggagcgaggttctgcttacccgaggccgctgctgttgcgg 60
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THE RESERVE TO COLOR OF THE PROPERTY OF THE PR
                                                                                                                                       This sequence represents a nucleic acid molecule designated Gene 47 from CC the human cDNA clone HOGAV75 (deposited as clone ATCC 97897 and ATCC 209043) which encodes a secreted human protein. The gene can be used to CC immunoglobulin FC portion (e.g. AAV59502) for increasing the stability of CC immunoglobulin FC portion (e.g. AAV59502) for increasing the stability of CC the fused protein as compared to the human protein only.

CC The invention relates to 186 novel genes and their fragments (nucleic CC which are useful for preventing, treating or ameliorating medical CC conditions e.g. by protein or gene therapy. Also, pathological CC conditions can be diagnosed by determining the amount of the new CC conditions can be diagnosed by determining the presence of mutations in CC the new polynucleotides. Specific uses are described for each of the 186 CC the new polynucleotides. Specific uses are described for each of the 186 CC conditions of the presence of mutations in CC polynucleotides, based on which tissues they are most highly expressed in CC conditions for described needs.
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Kyaw H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New isolated human genes and the secreted polypeptide(s) they encode - useful for diagnosis and treatment of e.g. cancers, neurological disorders, immune diseases, inflammation or blood disorders
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                                                                                                               (see AAV59511 for described uses).
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Greene JM,
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Query Match Best Local Similarity Sequence 1196 BP; 360 A; 212 C; 259 G; 61.1%; Score 895; Pred. No. 0; 364 T; 1 other; DB 19; Length 1196;

Q Qy Вþ δÃ В δ. Ъ Q 망 Dp QΥ ДĎ ρy Db Qy 밁 Matches 1065; 230 184 170 124 110 350 304 290 244 caaagacagggtgttccaatgaattcactcaggtttctcttttgagggtcagagaattgct 410 470 364 64 cccccgggtgaagccaccgtcatcatgtctgaccaggaggcaaaaccttcaactgaggac 123 50 4 gaaggatttgtaaaccccggagcgaggttctgcttacccgaggccgctgctgctgtgcggaga 63 gaaggatttgtaaaccccggagcgaggttctgcttacccgaggccgctgctgtgcggaga 109 ${\tt caaagacagggtgttccaatgaattcactcaggtttctcttttgagggtcagagaattgct}$ gagattcacttcaaagtgaaaatgacaacacatctcaagaaactcaaagaatcatactgt gagattcacttcaaagtgaaaatgacaacacatctcaagaaactcaaagaatcatactgt 243 ttgggggataagaaggaaggtgaatatattaaactcaaagtcattggacaggatagcagt 229 ttgggggataagaagcaaggtgaatatattaaactcaaagtcattggacaggatagcagt 183 cccccgggtgaagccaccgtcatcatgtctgaccaggaggcaaaaccttcaactgaggac 169 aatccttttttatttttaaaaatagttcttttgtaatgtggtgttcaaaaacggaattgaa ${\tt aatcctttttattttaaaaaatagttcttttgtaatgtggtgttcaaaacggaattgaa}$ Conservative 0; Mismatches 1; Indels 1; Gaps 289 349 303 589 469 423

(HUMA-) HUMAN GENOME

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                                                                                                                                                                                                                                 Human; secreted protein; fusion protein; gene therapy; protein therapy; diagnosis; tissue; cancer; tumour; neurodegenerative disorder; leukaemia; developmental abnormality; foetal deficiency; blood; allergy; renal; ds; immune system; asthma; lymphocytic disease; brain; hepatic; lymphoma; inflammation; ischaemic shock; Alzheimer's disease; restenosis; AIDS; cognitive disorder; schizophrenia; prostate; obesity; osteoclast; thymus;
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The invention relates to 186 novel genes and their fragments (nucleic acid sequences: AAV59511-V59812; amino acid sequences AAV74731-W75026) which are useful for preventing, treating or amedicating medical
                                                                                                                                                                                                                                                                                                                                              conditions e.g. by protein or gene therapy. Also, pathological conditions can be diagnosed by determining the amount of the new polypeptides in a sample or by determining the presence of mutations in the new polynucleotides. Specific uses are described for each of the 186 polynucleotides, based on which tissues they are most highly expressed in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New isolated human genes and the secreted polypeptide(s) they encode - useful for diagnosis and treatment of e.g. cancers, neurological disorders, immune diseases, inflammation or blood disorders
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P-PSDB; AAW74777.
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e PA, Ni J, Olsen HS,
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                                                                                                sentrin nucleotide sequence.
  Location/Qualifiers
                                                                                                                                                                                  cDNA; 1514 BP
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches 670;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present invention describes an antisense compound (I) 8-30 nucleotides long targeted to a nucleic acid molecule encoding human sentrin. The antisense compound comprises a phosphorothicate antisense oligonucleotide which inhibits expression of human sentrin. (I) is useful for inhibiting expression of sentrin in human cells or tissues in vitro, for treating humans or other animals suspected of having or being prone to a disease associated with sentrin expression. (I) can also be used for research or diagnostic purposes. The present sequence encodes human sentrin.
470 tcaatccttttttatttttaaaaatagttcttttgtaatgtggtgttcaaaacggaattg
               422 tcaatccttttttatttttaaaaatagttcttttgtaatgtggtgttcaaaacgggaattg
                                                               410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 1514 BP; 462 A; 256 C; 314 G; 482 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 13; Column 39-42; 29pp; English.
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                                                                                                                                                                                                                     gtgagattcacttcaaagtgaaaatgacaacatctcaagaaactcaaagaatcatact
                                                        ctgataatcatactccaaaagaactgggaatggaggaagaagatgtgattgaagtttatc
                                                                                                                                                                gtcaaagacagggtgttccaatgaattcactcaggtttctcttttgagggtcagagaattg
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99.9%;
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Pred. No. 2.2e-282;
0; Mismatches 1;
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RESULT
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                                    This sequence represents a human nucleotide sequence which is differentially expressed in colon cancer cells compared to the expression levels in normal cells. The nucleotide sequence can be used as a source of primers and probes. The nucleotide sequence is useful for determining the phenotype of a cell by detecting the differential expression of the sequence relative to a normal cell. The probes derived from the sequence can also be used to determine the phenotype of cells in a sample. Probes and antibodies which hybridise to the nucleotide sequence can also be used to determine the phenotype of cell. The primers are useful for detecting a mutation in a test nucleotide sequence and also for detecting cancer, preferably colon cancer. Antibodies against the protein encoded by the nucleotide sequence can also be used in a method to detect colon cancer. The diagnostic method is non-invasive and accurate for diagnosing
                            colon cancer at an early stage.
                                                                                                                                                                                                                                                                                     Claim 16; Page 211-212; 345pp; English.
                                                                                                                                                                                                                                                                                                                      Novel nucleic acids and proteins for identifying therapeutic agents useful for treating and diagnosing cancer, especially colon cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                Endege WO,
Catino TJ,
                                                                                                                                                                                                                                                                                                                                                                             WPI; 2000-256641/22.
                                                                                                                                                                                                                                                                                                                                                                                                                Schlegel R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (FARB ) BAYER CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 31-AUG-1998;
27-JAN-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    detect mutation; non-invasive diagnostic method;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human colon cancer differentially expressed nucleotide sequence #220.
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99US-0117393
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                                                                                                                                                                                                                                                                                                                                                                                                                            KE, Astle JH, Burgess CC,
, Ford DM, Lewis ME, Molii
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                                                                                                                                                                                                                                                                                                                                                                                                                                           Carroll E;
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Sequence 616 BP;

181 A; 109 C; 149 G; 170

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17-AUG-1997 (first entry)
             nucleoprotein (NP) and which may be accessory proteins required for influenza virus replication. NPI-6 was identified as a novel protein sequence. NPI sequences were isolated by interactive trap selection using LexA-NP as bait and yeast transformed with an HeLa CDNA library. NPI-1 (see also AAT63334) and NPI-2 to NPI-6 CDNAs we cloned and analysed. The clones can be used to produce human NPI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
                                                                                                           cDNA clones (AAT63335-39) comprise partial sequences for human nucleoprotein interactor proteins NPI-2 to NPI-6, respectively. These are host cell proteins which interact with influenza virus
                                                                                                                                                                                                                                                                                                                                                                06-OCT-1995;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            W09712967-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Host cell protein; NPI-6; nucleoprotein interactor
influenza virus; replication; antiviral; virucide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                103
                                                                                                                                                                                                    New isolated DNA which encodes viral interacting proteins - used in assays to isolate products for inhibiting viral protein binding which is required for infection, replication, assembly or release
                                                                                                                                                                                                                                                                                                    Oneill R,
                                                                                                                                                                                                                                                                                                                                (MOUN ) MOUNT SINAI MEDICAL CENT
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 proteins for use in identifying cpds. that inhibit viral
                                                                                                                                                                        Disclosure; Fig 11; 98pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            343 gataatcatactccaaaagaactgggaatggaggaagaagatgtgattgaa 393
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                                                                                                                                                                                                                                                                                                                                                                   95WO-US13044.
                                                                                                                                                                                                                                                                                                                                                                                                   95WO-US13044.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99.78;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pred. No. 1.2e-131; 0; Mismatches 1;
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AAF59399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT
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Best Local S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 372 BP; 121 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         replication
                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAF59399;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAF59399 standard; DNA;
                                                                                                                                                                                                                                                                                                                                                                                                    Human host cell protein NPI-6 partial nucleotide sequence SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                                 02-MAY-2001 (first entry)
         The present invention describes a method (M1) for identifying a substance that inhibits the interaction of a viral protein (VP) with a host cell protein (HP). The method comprises: (a) contacting HP with VI
                                                                                                                                                                         O'Neill R,
                                                                                                                                                                                                                                                                                                             WO200111335-A2
                                                                                                     Identifying a substance that inhibits the interaction between a viral protein and a host cell protein, useful for the discovery of new
                                                                                                                                                                                                                             11-AUG-1999;
                                                                                                                                                                                                                                                        11-AUG-2000; 2000WO-US22257
                                                                                                                                                                                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                        Identification; antiviral; viral protein; viral replication; NP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             181
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                                                               Disclosure; Fig 11; 147pp; English
                                                                                           antiviral compounds
                                                                                                                                              WPI; 2001-168816/17.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ggataagaaggaaggtgaatatattaaactcaaagtcattggacaggatagcagtgagat 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       acagggtgttccaatgaattcactcaggtttctcttttgagggtcagagaattgctgataa 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              334;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      tcatactccaaaagaactgggaatggaggaagaag
                                                                                                                                                                                                                                                                                                                                                              infection; nucleoprotein;
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                                                                                                                                                                                                                               99US-0148263
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99.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        372
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Pred. No. 4.2e-124;
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Best Local
           (WEIN/) WEINWURZEL H.

(YEDA ) YEDA RES & DEV CO LTD
                                                                  11-MAY-1994;
                                                                                 02-OCT-1994;
                                                                                                                    11-MAY-1995;
                                                                                                                                                         23-NOV-1995
                                                                                                                                                                                         W09531544-A1
                                                                                                                                                                                                                                                                      Tumour necrosis factor receptor; TNF-R; p55IC; Fas-IC;
                                                                                                                                                                                                                                                                                                          TNF-R p55IC/Fas-IC-binding protein DD11 cDNA clone.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     where the ability of the test substance to inhibit HP/VP interaction is indicated by a decrease in complex formation. The antiviral compounds that inhibit the interaction between a host protein (NSI-BP or NPI-1) and a viral protein (NSI) are useful for treating or inhibiting viral infection, preferably influenza and rhabdovirus infection, in humans. Antiviral compounds include peptides and antibodies. In particular compositions comprising a polypeptide containing an amino acid sequence corresponding to the NP-NLS domain of the influenza virus NP protein, which inhibits the specific interaction of the NPI-1 protein with the influenza virus NP protein are useful for treating or inhibiting influenza virus (NP protein are useful for treating or inhibiting influenza virus (NP protein are useful for treating or inhibiting influenza virus (NP protein are useful for treating or inhibiting influenza virus (NP protein APP in present sequence represents a human host cell protein (NPI-6 partial nucleotide sequence, which is used in the exemplification of the present invention.
                                                                                                                                                                                                                                                             intracellular
                                                                                                                                                                                                                                                                                                                                               26-MAR-1996 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                   AAT03735 standard; cDNA; 425 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     181
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       tcatactccaaaagaactgggaatggaggaagaag 343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  acagggtgttccaatgaattcactcaggtttctcttttgagggtcagagaattgctgataa
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              334;
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                                                                                                                                                                                                                                                           domain
                                                              94IL-0111125.
94IL-0109632.
                                                                                                                    95WO-US05854.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            19.48;
99.78;
                                                                                                                                                                                                                                                  binding protein; ss
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Pred. No. 4.2e-124;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 372;
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WPI; 1995-206931/27
                               Matsubara K, Okubo K;
                                                                 (MATS/) MATSUBARA K. (OKUB/) OKUBO K.
                                                                                                                  12-NOV-1993;
                                                                                                                                                   11-NOV-1994;
                                                                                                                                                                                   01-JUN-1995
                                                                                                                                                                                                                    WO9514772-A1
                                                                                                                                                                                                                                                  Homo sapiens.
                                                                                                                                                                                                                                                                                            Gene signature; messenger RNA; mRNA; relative abundance; frequency; human; cloning; mapping; non-biased library; diagnosis; detection;
                                                                                                                                                                                                                                                                                                                                                   Human gene signature HUMGS00738.
                                                                                                                                                                                                                                                                                                                                                                                                                    AAT19668;
                                                                                                                                                                                                                                                                                                                                                                                   28-JUN-1996 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                AAT19668 standard; cDNA to mRNA; 180 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cDNA clone DD11 (AAT03735) was isolated by screening a human HeLa library using the human tumour necrosis factor receptor (TNP-R) p55 death domain (p55DD) as 'bait'. The full length of the DD11 transcript is approx 1.2 kb. The protein encoded by cDNA DD11 interacts strongly with p55DD (amino acids 326-414) and also with human and mouse FAS intracellular domain. Such proteins may
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 425 BP; 135 A; 80 C; 115 G; 95 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   be used modulate TNF-R function.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 18; Fig 12; 96pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TNF-NGF receptor superfamily intracellular domain-binding proteins useful for modulating receptor function, e.g. for treating tumours or HIV-infected cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1996-010930/01.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   351 aagaactgggaatggag 367
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                260 caatgaattcactcaggtttctctttgagggtcagagagttgctggataatcatactccaa 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           231 tgaaaatgacaacacatctcaagaaactcaaagaatcatactgtcaaagacagggtgttc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                abnormal cell function; ss.
                                                                                                                  93JP-0355504
                                                                                                                                                  94WO-JP01916.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13.4%;
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CC double-stranded DNA (or its complementary strand or the corresp. CC double-stranded DNA) which comprises one of the 7837 "GS" sequences CC given in AAT19001-T26837 and which is able to hybridise to part of thuman genomic DNA, cDNA or mRNA is claimed. The GS (Gene Signature) CC thuman genomic DNA, cDNA or mRNA is claimed. The GS (Gene Signature) CC sequences were obtained from 3'-directed cDNA libraries prepared CC from various human tissues; synthesis of cDNA was initiated from the CC intranslated sequence is unique to a particular mRNA species, almost CC untranslated sequence is unique to a particular mRNA species, almost CC all the 3'-oriented cDNAs hybridise with specific mRNAs. Each library CC is constructed so as to reflect accurately the relative abundance of CC different mRNAs in the particular tissue from which it was derived. CC The appearance frequency of a given GS in a cDNA library can be CC determined (esp. using primers and probes derived from the GS CC sequences) as a means of diagnosing abnormal cell function or for CX or cognising different cell types.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; Page 445; 2245pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Identifying gene signatures in 3'-directed human cDNA library - e.g. for diagnosis of abnormal cell function, by preparing cDNA that reflects relative abundance of corresp. mRNA in specific human
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Sequence 180 BP; 65 A; 26 C; 26 G; 63 T; 0 other;

Дb δÃ B Ş Query Match 5.8%; Score 85; DB 16; Length 180; Best Local Similarity 100.0%; Pred. No. 2.4e-30; Matches 85; Conservative 0; Mismatches 0; Indels 1131 cttcattaaaataaacaatatttgt 1155 1071 gattttatttgtactttttggcctgggatatgggttttaaatggacattgtctgtaccag 1130 144 cttcattaaaataaacaatatttgt 168 84 gattttatttgtactttttggcctgggatatgggttttaaatggacattgtctgtaccag 143 0; Gaps 0

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BP 191 91006 EVRY cedex - France
Email: segref@genoscope.cns.fr. Web : www.genoscope.cns.fr.
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http://fulllength.invitrogen.com*

2 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /tissue_type="neuroblastoma cells"
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RESULT AL528799

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                                                        ttcaggcttgtggtgataaataagatcgaccaatgcaagtgttcataatgactttccaat
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: segref@genoscope.cns.fr, Web : www.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Li,W.B., Gruber,C., Jessee,J. and Polayes,D. Full-length cDNA libraries and normalization Unpublished (2001)
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AL544942 LTI_NFL006_PL2 Homo sapiens cDNA clone CSODI012VA10 5
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1 (bases 1 to 898)
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AL544942
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1 160 c 200 g 275 t
                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone_lib="LTI_NFL006_PL2"
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99.9%;
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Pred. No. 0;
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                                                                                                                                 Li, W.B., Gruber, C., Jessee, J. and Polayes, D. Full-length cDNA libraries and normalization Unpublished (2001)
Contact: Genoscope
                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 907)
                                                                                                                                                                                                                                                                                                     prime, mRNA sequence.
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AL533666 LTI_FL013_FBrn1 Homo sapiens cDNA clone CS0DF002Y003 5
                                                                                        BP 191 91006 EVRY cedex - France Email: segref@genoscope.cns.fr. Web : www.genoscope.cns.fr.
                                                                                                                      Genoscope - Centre National de Sequencage
                                                                                                                                                                                                                                           Homo sapiens
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/db_xref="taxon:9606"
/clone="CSODF002Y003"
/clone_lib="LTI_FL013_FBrn1"
                                                                           Location/Qualifiers
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166 c 206 g 280 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        pCMVSPORT 6 vector. Library was constructed by Life
Technologies. Contact: Feng Liang Life Technologies, a
division of Invitrogen 9800 Medical Center Drive Rockville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="Organ: Fetal brain; Vector: pCMVSPORT 6; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the control of the control of the Not I are constructed by Life
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week, 24 week and 26 week)"
/lab_host="DH10B"
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99.9%;
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Pred. No. 0;
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Best Local Similarity
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                                                                             tccaaaagaactgggaatggaggaagaagatgtgattgaagtttatcaggaacaaacggg
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Genoscope - Centre National de Sequencage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Full-length cDNA libraries and normalization Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Li, W.B., Gruber, C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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AL583458 LTI_NFL010_BC2 Homo
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/note="Vector: pcMVSpOR7 6; Site_1: Not1; lst strand cDNA
/note="Vector: pcMVSpOR7 6; Site_1: Not1; lst strand cDNA
was primed with a Not1-oligo(dT) primer. Five prime end
enriched, double-stranded cDNA was digested with Not I and
cloned into the Not I and Eco RV sites of the pcMVSpOR7 6
vector. Library was normalized. Library was constructed by
Life Technologies, Contact : Feng Liang Life Technologies,
a division of Invitrogen 9800 Medical Center Drive
Rockville, Maryland 20850, USA Fax : (1) 301 610 8371
Email : fliang@lifetech.com URL :
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166 c 199 g 279 t
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/clone_lib="LTI_NFL010_BC2"
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/db_xref="taxon:9606"
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 Mismatches

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Pred. No. 0;
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1 (Dases 1 to 868)

Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
Unpublished (2011)
Contact: Genoscope
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              prime, mRNA sequence.
AL521484
AL521484.1 GI:12784977
EST.
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AL521484 LTI_NFL004_NBC2 Homo sapiens cDNA clone CS0DB001YN17 5
                                                                                                                                                                                                                                                                                                                                                           BP 191 91006 EVRY cedex - France
Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
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/note-*Organ: brain; Vector: pCMVSPORT 6; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the NotI and Eco RV sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies. Contact: Feng Ling Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockwille, Maryland 20850, USA Fax: (1) 301 610 8371 Email: fliang@lifetech.com URL:
                                                                                                                                                                                 /tissue_type="neuroblastoma cells"
/lab_host="DH10B"
                                                                                                                                                                                                                                                             /db_xref="taxon:9606"
/clone="CS0DB001YN17"
                                                                                                                                                                                                                        /sex="male"
                                                                                                                                                                                                                                            /clone_lib="LTI_NFL004_NBC2"
                                                                                                                                                                                                                                                                                                    /organism="Homo sapiens"
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                                                                    agatgacagataaggtgagagtaatgac 922
                                                                                                    AAGCTACTTTTAAAATTTGAGGGTCTGGACCAAAAGAAGAGGGAATATCAGGTTGAAGTCA
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                                                                                       304 gataatcatactccaaaagaactgggaatggaggaagaagatgtgattgaagtttatcag
                                                                                                                                                                                                         184 gagattcacttcaaagtgaaaatgacaacacatctcaagaaactcaaagaatcatactgt 243
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                                                                                                                                                                                                                                                                                                     124 ttgggggataagaagcaaggtgaatatattaaactcaaagtcattggacaggatagcagt 183
                                                                                                                                                                                                                                                                                                                                                                            85
                                                                                                                                                                                                                                                                                                                                                                                               64 cccccgggtgaagccaccgtcatcatgtctgaccaggaggcaaaaccttcaactgaggac 123
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4 gaaggatttgtaaaccccggaggcgaggttctgcttacccgaggccgctgctgtgcggaga 63
                                                                                                                                                                                                                                                                                                                                                                            CCCCCGGGTGAAGCCACCGTCATCATGTCTGACCAGGAGGCAAAACCTTCAACTGAGGAC
GATAATCATACTCCAAAAGAACTGGGAATGGAGGAAGAAGATGTGATTGAAGTTTATCAG
                                                                                                                                                                                      GAGATTCACTTCAAAGTGAAAATGACAACACATCTCAAGAAACTCAAAGAATCATACTGT
                                                                                                                                                                                                                                                                             TTGGGGGATAAGAAGGAAGGTGAATATTAAACTCAAAGTCATTGGACAGGATAGCAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  660;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: cgapbs-r@mail.nih.gov
Tissue Procurement: CLONTECH Laboratories,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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BG541610.1 GI:13533843
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Plate: LLCM1521 row: i column: 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cDNA Library Preparation: CLONTECH Laboratories, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /lab_host="DH10B (TI phage-resistant)"
/note="Organ: lung; Vector: pDNR-LIB (clontech); Site_1:
/note="Gran: lung; Vector: pDNR-LIB (clontech); Site_1:
/note="Gran: lung; Vector: pDNR-LIB (clontech); Site_1:
/note="Gran: lung; Vector: pDNR-LIB (gccattatggcc); 5' and
/note: adaptor: Site_2: Sifi (ggccattatggcc); 5' and
/note: dadptor: Sequence: 5'-cACGGCCATGTGGCC-3' and 3' adaptor sequence:
/note: 5'-cATGCTAGAGCCGCACATG-GT(30)BN-3' (where B = A,
/note: A = A, C, G, or T). Average insert size 1.9
/note: A = A, C, G, or T). Average insert size 1.9
/note: This library was enriched for full-length clones
/note: this is a NIH_MGC Library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone="IMAGE:4695641"
/clone_lib="NIH_MGC_77"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Homo sapiens"
/db_xref="taxon:9606"
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Pred. No. 4.1e-288;
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Matches 592; Query Match

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Score 592; DB 106; Pred. No. 2.7e-279; Mismatches

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AL532394
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Full-length cDNA libraries
Unpublished (2001)
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BP 191 91006 EVRY cedex - France
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1 (bases 1 to 756)
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                                                                                                                                                                                                                                                                                                                                                                                                           segref@genoscope.cns.fr,
                                                    vector. Library was normalized. Library was constructed by Life Technologies. Contact: Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville, Maryland 20850, USA Fax: (1) 301 610 8371 Email: fliang@lifetech.com URL:
                                                                                                                                                /note="Organ: brain; Vector: pCMVSPORT 6; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pCMVSPORT 6
                  http://fulllength.invitrogen.com"
140 c 161 g 236 t 1
                                                                                                                                                                                                                                                                       /sex="male"
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                                                                                                                                                                                                                                                                                       /clone_lib="LTI_NFL001_NBC4"
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                                                                                                                                                                                                                                   /lab_host="DH10B"
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                                                                                                                                                                                                                                 Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 858)
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BE888192.1 GI:10344249
                                                                                                                                                                                                                                                                                                                                                                                                                           BE888192 858 bp mRNA EST 20-OCT-2000 601511710F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3912914 5',
                                                                                                  found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Plate: LLAM9732 row: d column: 03
                                                                                                                                                                                                      Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
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National Institutes of Health, Mammalian Gene Collection (MGC)
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                                                                                                                                            cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:3912914"
/clone_lib="NIH_MGC_71"
                                                                      Location/Qualifiers
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                                                       NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, M
Unpublished (1999)
                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                                                                                       BE889687.1
                                                                                                                                                                                                                                                            mRNA sequence.
BE889687
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                                         Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                             Homo sapiens
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Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT
Average insert_size 2.1 kb. "
                                                                                                                                                                                                                                       GI:10347260
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                166 g
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                                                                                Mammalian
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                                                                                                                                          Hominidae;
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                                                                                  Collection (MGC)
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                                                                                                                                                             Euteleostomi;
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BASE COUNT
ORIGIN
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                    DEFINITION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                193 ttcaaagtgaaaatgacaacatctcaagaaactcaaagactatactgtcaaagacag
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                                                                                                                                                                                                                                                                                                                                                                                                         361
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 GTAAACCCCGGAGCGAGGTTCTGCTTACCCGAGGCCGCTGCTGTGCGGAGACCCCCGGGT 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  actccaaaagaactgggaatggaggaagaagatgtgattgaagtttatcaggaacaaacg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            glaaaccccggagcgaaggttctgcttacccgaggccgctgctgtgcggagacccccgggt
                                                                                                                                                                                                                             CCCATCTCTTTGAAACATCTGGTAATTTGAATTCTAGTGCTCATTATTCATTATTGTTTG
                                                                                                                                                                                                                                                     cccatctctttgaaacatctggtaatttgaattctagtgctcattattcattattgtttg
                                                                                                                                                                                                                                                                                                                 TTATTTTAAAAATAGTTCTTTTGTAATGTGGTGTTCAAAACGGAATTGAAAACTGGCAC
                                                                                                                                                                                                                                                                                                                                      ttatttttaaaaatagttcttttgtaatgtggtgttcaaaacgggaattgaaaactggcac
                                                                                                                                                                                                                                                                                                                                                                                                    GGTGTTCCAATGAATTCACTCAGGTTTCTCTTTGAGGGTCAGAGAATTGCTGATAATCAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAGAAGGAAGGTGAATATTAAACTCAAAGTCATTGGACAGGATAGCAGTGAGATTCAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     aagaagcaaggtgaatatattaaactcaaagtcattggacaggatagcagtgagattcac 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GAAGCCACCGTCATCATGTCTGACCAGGAGGCAAAACCTTCAACTGAGGACTTGGGGGAT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gaagccaccgtcatcatgtctgaccaggaggcaaaaaccttcaactgagggacttgggggat 132
                                                                                                                                            TTTTCATTGTGCTGATTTTTGGTGATCAAGCCTCAGTCCCCTTCATATT 589
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TTCAAAGTGAAAATGACAACACCTCAAGAAACTCAAAGAATCATACTGTCAAAGACAG
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mRNA
             BG169405 1166 bp
602320976F1 NIH_MGC_89
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Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM9735 row: C column: 06
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/clone_lib="NH_MCC_71"
/clone_lib="NH_MCC_71"
/tissue_type="leiomyosarcoma"
/lab_host="DH10B (phage-resistant)"
/note="Organ: uterus; Vector: pCMV-SPORT6; Site_1: Not1;
Site_2: Sall; cloned unidirectionally. Primer: Oligo dT
Average insert_size 2.1 kb. "
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99.8%;
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Pred. No. 8.5e-253;
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                 Homo sapiens cDNA clone IMAGE:4424131 5',
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ORGANISM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches 674;
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                     424
                                                         362
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                                                                          242 CAAAGACAGGGTGTTCCAATGAATTCACTCAGGTTTCTCTTTGAGGGTCAGAGAATTGCT
                                                                                                                                                                                                                                                                                        182 GAGATTCACTTCAAAGTGAAAATGACAACATCTCAAGAAACTCAAAGAATCATACTGT
                                                                                                                                                                                                                                                                                                                                                           62
                                                                                                                                                                                                                                                                                                                                                                                                                                                         64 cccccgggtgaagccaccgtcatcatgtctgaccaggaggcaaaaccttcaactgaggac 123
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gataatcatactccaaaagaactgggaatggaggaagaagatgtgattgaagtttatcag
                                                                                                                                                                                                                                caaagacagggtgttccaatgaattcactcaggtttctctttgagggtcagagaattgct
                                                                                                                                                                                                                                                                                                       gagattcacttcaaagtgaaaatgacaacacatctcaagaaactcaaagaatcatactgt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GAAGGATTTGTAAACCCCGGAGCGAGGTTCTGCTTACCCGAGGCCGCTGCTGTGCGGAGA 61
                                                         GATAATCATACTCCAAAAGAACTGGGAATGGAGGAAGAAGATGTGATTGAAGTTTATCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                      CCCCCGGGTGAAGCCACCGTCATCATGTCTGACCAGGAGGCAAAACCTTCAACTGAGGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     http://image.llnl.gov
Plate: LLAMI0167 row: h column:
High quality sequence stop: 672.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CDNA Library Preparation: Life Technologies, Inc. CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL). DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tissue Procurement: ATCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /tissue_type="hypernephroma, cell line"
/lab_bost="hyll0B (phage=resistant)"
/note="Organ: kidney; Vector: pcMV-SPORT6; Site_1: NotI;
Site_2: Sall; Cloned unidirectionally; oligo-dT primed.
Average insert size 1.3 kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."

197 c 282 g 318 t 1 others
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/db_xref="taxon:9606"
/clone="IMAGE:4424131"
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99.6%;
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Pred. No. 6.3e-246;
0; Mismatches 3;
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FEATURES
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                                                                                           gacccccgggtgaagccaccgtcatcatgtctgaccaggaggcaaaaccttcaactgagg 121
                                                                                                                                                           GGGAAGGATTTGTAAACCCCGGAGCGAGGTTCTGCTTACCCGAGGCCGCTGCTGTGCGGA 67
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Tel: 86-21-50801919(ex.45)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
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Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
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clone is available at CHGC in Shanghai.
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                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                              /note="Vector: pTriplEx2; Site_1: sfiIA; Site_2: sfiIB1" 127 c 155 g 213 t 2 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone="FHTAAAH02"
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                                                                                                                                                                                                                                                                                                                                                                                                                                            /tissue_type="hypothalamus"
/dev_stage="Fetal"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone_lib="FHTA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: cgapbs-r@mail.nih.gov
Tissue Procurement: CLONTECH Laboratories, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; 1 (Dases 1 to 850)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collect
                                                                                                                                                                                                                                                                                                                                                         found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov plate: LLCM1259 row: e column: 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
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/clone="IMAGE:456534"
/clone=lib="NIH_MCC_75"
/clone=lib="NIH_MCC_75"
/lab_host="DH10B (T1 phage-resistant)"
/note="Organ: kidney; Vector: pDNR-LIB (Clontech); Site_1:
/note="Organ: kidney; Vector: pDNR-LIB (Clontech); S' and
Sill (ggccgctcggcc); Site_2: Sfil (ggccattafgcc); S' and
3' adaptors were used in cloning as follows: 5' adaptor sequence:
5'-CACGGCCATTATGGCC-3' and 3' adaptor sequence:
5'-CACGGCCGACATG-dT(30)BN-3' (where B = A,
C, or G and N = A, C, G, or T). Average insert size 1.65
kb (range 0.5-4.0 kb). 15/15 colonies contained inserts
by PCR. This library was enriched for full-length clones
                                                                                                                                                                                                                                                  /db_xref="taxon:9606"
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BG528729.1
                                                                                                         Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 769)
                                                                                                                                                                                                                               BG528729 769 bp mRNA F 602579628F1 NIH_MGC_60 Homo sapiens cDNA
                                     Contact: Robert Strausberg, Ph.D Email: cgapbs-r@mail.nih.gov Tissue Procurement: DCTD/DTP
                                                                             Unpublished (1999)
                                                                                      NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
                                                                                                                                                                                                                       mRNA sequence.
cDNA Library Preparation: CLONETECH Laboratories, cDNA Library Arrayed by: The I.M.A.G.E. Consortium DNA Sequencing by: Incyte Genomics, Inc.
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Pred. No. 3.7e-234;
0; Mismatches 1;
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                                                                                        AACTGGCACCCCATCTCTTTGAAACATCTGGTAATTTGAATTCTAGTGCTCATTATTCAT
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/clone_lib="NIH_MGC_50"
/tissue_type="adenocarcinoma"
/lab_host="DH10B (Tl phage-resistant)"
/lab_host="DH10B (Tl phage-resistant)"
/lab_host="bH10B (Tl phage-resistant)
/lab_host="bh10B (Tl p
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/db_xref="taxon:9606"
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Pred. No. 3.6e-233;
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                                                                                                                                                                                                                           TTGGGGGATAAGAAGGAAGGTGAATATTAAACTCAAAGTCATTGGACAGGATAGCAGT 215
                                                                              GAGATTCACTTCAAAGTGAAAATGACAACACATCTCAAGAAACTCAAAGAATCATACTGT 275
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Plate: LLCM1496 row: p column: 05 High quality sequence stop: 800.
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National Institutes of Health, Mammalian Gene Collection (MGC)
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1 (bases 1 to 822)
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Clone distribution: MGC clone distribution information can be
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/clone_lib="NMGE.59"
/clone_lib="NMGE.59"
/clone_lib="Mucoepidermoid carcinoma"
/lab_bost="DH10B (T] phage-resistant)"
/lab_bost="DH10B (T] phage-resistant)"
/lab_bost="DH10B (T] phage-resistant)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: cgapbs-remail.nih.gov
Tissue Procurement: CLONTECH Laboratories, Inc.
cDNA Library Preparation: CLONTECH Laboratories, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
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Plate: LLCM1515 row:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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                                                       /clone_"IMAGE:4693352"
/clone_lib="NIH_MGC_77"
/lab_host="pH10B (T1 phage-resistant)"
/lab_host=
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                               679 TTCAGGCTTGTGGTGATAAATAAGATCGACCAATGCAAG 717
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Search completed: August 17, Job time: 4517 sec

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